SEQUENCE LISTING

5	(1) GENE	RAL INFORMATION:
J	(I)	APPLICANT: Vreeland, Valerie, Ng, Kwan
10		TITLE OF INVENTION: Recombinant Vanadium Haloperoxidases d Their Uses
10	(iii)	NUMBER OF SEQUENCES: 2
	(iv)	CORRESPONDENCE ADDRESS:
15		(A) ADDRESSEE: Townsend and Townsend and Crew LLP (B) STREET: Two Embarcadero Center, Eighth Floor (C) CITY: San Francisco
		(D) STATE: California
		(E) COUNTRY: USA (F) ZIP: 94111-3834
20	(12)	COMPUTER READABLE FORM:
	(•)	(A) MEDIUM TYPE: Floppy disk
		(B) COMPUTER: IBM PC compatible
٠ <u>. ا</u>		(C) OPERATING SYSTEM: PC-DOS/MS-DOS
190 117 125		(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
	(vi)	CURRENT APPLICATION DATA:
1000		(A) APPLICATION NUMBER: US Not yet assigned
- 		(B) FILING DATE: 08-AUG-1998
		(C) CLASSIFICATION:
a State	(viii)	ATTORNEY/AGENT INFORMATION:
į		(A) NAME:
		(B) REGISTRATION NUMBER:
35		(C) REFERENCE/DOCKET NUMBER: 023070-087100US
	(ix)	TELECOMMUNICATION INFORMATION:
		(A) TELEPHONE: (415) 576-0200
		(B) TELEFAX: (415) 576-0300
40		
	(2) INFO	RMATION FOR SEQ ID NO:1:
	(i)	SEQUENCE CHARACTERISTICS:
45		(A) LENGTH: 2931 base pairs .
		(B) TYPE: nucleic acid
		(C) STRANDEDNESS: single
		(D) TOPOLOGY: linear
50	(ii)	MOLECULE TYPE: cDNA
	(ix)	FEATURE:
		(A) NAME/KEY: CDS
55		(B) LOCATION: 2282258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	CGCGGACAAG	CCTTGGAAGA	GAGGTTGCCC	AATTCAACAG	AGCGAGGCCC	GTGAAGGTGT	60
5	GGAGGACACG	TGCTACAAGC	TGATCCACGA	GAGCCTCAAC	TTCCCTACTG	ATACGGGAGT	120
	THETT A CHECK	CCGCGTTGCC	AAAAACCGCA	מריידים ממרמ	GCGCTCGCGA	GCGCCACATG	181

	CTT	CCCA -	.CGC	ATCC	ACAA	AA T	CGAC	AGTG	G TA	TCGC	TGAG -	CTT	GAAT		Leu	TGC Cys	236
5													GAC Asp			GTG Val	284
10		Arg														CAG Gln 35	332
15	_												GAG Glu				380
2 20													GTT Val				428
120 120 120 120													ATT Ile 80				476
0125 1125							_						GCA Ala				524
1 30			-										GAG Glu				572
35													AAC Asn				620
40													GTA Val				668
.0													ACA Thr 160				716
45													ATG Met				764
50													GAC Asp				812
55													ATT Ile				860
	GTG	CCT	GCG	GGA	GAC	CCG	GCG	GGT	CGC	CTC	GTC	AAT	CCT	ACC	GCT	GCG	908

	Val	Pro	Ala	Gly 215	Asp	Pro	Ala	Gly	Arg 220		Val	Asn	Pro	Thr 225	Ala	
5					ATA Ile				Ala						CCC Pro	956
10					CTT Leu											1004
15					GCG Ala											1052
					ACC Thr 280											1100
20 =					CTG Leu											1148
₩25		_			CAG Gln					_						1196
- 	_				TCT Ser											1244
35					CCG Pro											1292
33					GAC Asp 360											1340
40					GAG Glu											1388
45					AGG Arg											1436
50					CTT Leu											1484
م م					CCA Pro											1532
55					TCT Ser											1580

GCG CAG CGT GCC TCG TGT TAC CAA AAG TGG CAG GTG CAT CGA TTT GCA Ala Gln Arg Ala Ser Cys Tyr Gln Lys Trp Gln Val His Arg Phe Ala CGC CCC GAG GCT CTC GGG GGT ACC CTC CAC AAC ACC ATC GCG GGG GAT Arg Pro Glu Ala Leu Gly Gly Thr Leu His Asn Thr Ile Ala Gly Asp CTA GAT GCA GAC TTC GAC ATC TCC CTT CTT GAA AAT GAT GAG CTC TTG Leu Asp Ala Asp Phe Asp Ile 5er Leu Leu Glu Asn Asp Glu Leu Leu AAA CGT GTG GCG GAG ATA AAT GCG GCG CAG AAT CCC AAC AAC GAG GTC Lys Arg Val Ala Glu Ile Asn Ala Ala Gln Asn Pro Asn Ash Glu Val ACC TAC CTT CTT CCA CAA GCT ATC CAA GTG GGA TCG CCA ACG CAC CCT Thr Tyr Leu Leu Pro Gln Ala Ile Gln Val Gly 5er Pro Thr His Pro 11 125 TCC TAC CCG TCC GGC CAC GCT ACC CAA AAT GGA GCA TTT GCC ACA GTT Ser Tyr Pro Ser Gly His Ala Thr Gln Asn Gly Ala Phe Ala Thr Val IJ CTG AAG GCC CTC ATT GGC CTA GAT CGG GGA GGT GAG TGC TTC CCT AAC Leu Lys Ala Leu Ile Gly Leu Asp Arg Gly Gly Glu Cys Phe Pro Asn CCC GTG TTC CCA AGC GAT GAC GGC CTG GAA CTA ATC AAC TTC GAA GGG · 1964 Pro Val Phe Pro Ser Asp Asp Gly Leu Glu Leu Ile Asn Phe Glu Gly 1.4 GCA TGC CTT ACA TAT GAG GGA GAG ATC AAC AAG CTC GCG GTC AAC GTC Ala Cys Leu Thr Tyr Glu Gly Glu Ile Asn Lys Leu Ala Val Asn Val GCA TTT GGG AGG CAG ATG CTG GGC ATC CAC TAT CGG TTC GAC GGT ATC Ala Phe Gly Arg Gln Met Leu Gly Ile His Tyr Arg Phe Asp Gly Ile CAA GGC CTA CTT CTC GGA GAG ACA ATC ACT GTA CGA ACA CTT CAC CAG Gln Gly Leu Leu Gly Glu Thr Ile Thr Val Arg Thr Leu His Gln GAG CTG ATG ACG TTC GCC GAG GAA GCC ACC TTT GAA TTC CGC TTA TTC Glu Leu Met Thr Phe Ala Glu Glu Ala Thr Phe Glu Phe Arg Leu Phe ACC GGA GAG GTC ATC AAA CTT TTC CAG GAC GGG ACA TTC TCC ATC GAT Thr Gly Glu Val Ile Lys Leu Phe Gln Asp Gly Thr Phe Ser Ile Asp GGA GAT ATG TGT TCC GGT TTG GTT TAC ACT GGC GTG GCG GAC TGC CAG

Gly Asp Met Cys 5er Gly Leu Val Tyr Thr Gly Val Ala Asp Cys Gln

	GCT TAGTGCA	AGAA AATAATA	AATT GTCGGAT	GCT TAAAATO	GCAC CCACGAC	CCAA	2305
5	GTCGTCGAGT	CACGTCGCCG	GAGCATCCTT	CAGCGAAAAA	GGAGAGTAAC	CTATATGCTA	.2365
	TAGAGGAGAA	CCACGGAGTA	CAATGCAGGT	TCTTTTACCA	TGTACATTGG	ATTGCAGTAA	2425
	GTGCGGTTAG	AGAGGGATAC	GTTAAACGTG	CTTGCCTGTG	TATATGATAC	ATTTGTCATG	2485
10	GAAATATTAG	AATGCGTTGA	CTTGACTTCA	CCATGAAATA	CCATGATCGC	GTGGTGTGCT	2545
	GCTTTCACCT	GTCGGAGCGG	TACGTAAGAT	GTGCTTTCTA	CTGAGCCGTT	TGTGTTTAGT	2605
15	CCATTCCGCG	TGGCAGTGTA	AACAAAGAGG	ATGTAGTCTC	GCCCTCAGTT	TGGAGAGTAC	2665
	CGTAGGTGGC	AGGACGTATA	TCTCTGGTAG	CGGTCTGTTA	AGAACTTCCA	CAAGACCGTT	2725
	TACGTTTGGT	TGTTTAGTCG	ATGCCTCTTC	GTTACTTGAC	CGATCCATTG	AGAGTACCTG	2785
120 11	TACCAGTATG	GTGTAAGACA	TATTTTTCTC	CTGTTATGGA	TCTGTAGAAC	AGCTAGGTGT	2845
	TGTTTTATAC	ACAGGATGCT	ATAAAATAGG	GATGTTGATA	ATGGCATCGG	TACTCATGAA	2905
1725 113	ACCGCAAAAT	GGCGATAGAT	ATTCCC				2931
11						,	
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4	5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 676 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear															
		z.	. {	ii)	MOLE	CULE	TYP	E: p	rote	in						,	
1	10		(:	xi)	5EQU	ENCE	DE5	CRIP'	TION	: SE	Q ID	ио:	2 _. :				
		Met 1	Leu	Cys	His	Ala 5	Ala	Asp	Thr	Thr	Arg 10	Gly	Ser	Pro	Met	Pro 15	Asp
]	.5	Thr	Gly	Val	Leu 20	Arg	Leu	Leu	Thr	5er 25	Glu	Gln	Arg	Ala	Lys 30	Gly	Trp
	.	Arg	Arg	Gln 35	Leu	Glu	Gly	Glu	Lys 40	5er	Leu	Gly	Phe	His 45	Pro	Ser	Glu
	.0	Thr	Pro 50	Tyr	Ile	Lys	Tyr	Leu 55	Glu	Gly	Ser	Glu	Thr 60	Trp	Lys	Lys	Val
1 1 1	25	Lys 65	Leu	Pro	Thr	Asp	Gly 70	Ile	Ser	Ala	Ser	Lys 75	Ile	Leu	Gly	Lys	Ile 80
	•	Met	Ala	Arg	Val	Arg 85	Ile	Ala	Thr	Ala	Leu 90	Ala	Val	Val	Leu	Ala 95	Ala
74 3 14	0	Pro	Cys	Leu	Ala 100	Phe	Asp	Glu	Val	Thr 105	Ala	Ser	Gly	Val	Phe 110	Pro	Glu
1 1 2	_	Glu	His	Lys 115	His	Thr	Gly	Glu	Gly 120	Arg	His	Leu	Gln	Thr 125	Cys	Thr	Asn
J	5	Ser	Asp 130	Asp	Ala	Leu	Asp	Pro 135	Thr	Ala	Pro	Asn	Arg 140	Arg	Asp	Asn	Val
4	0	Ala 145	Phe	Ala	Ser	Arg	Arg 150	Asp	Ala	Ala	Arg	Arg 155	Glu	Arg	Asp	Gly	Thr 160
		Gly	Thr	Val	Cys	Gln 165	Ile	Thr	Asn	Gly	Glu 170	Thr	Asp	Leu	Ala	Thr 175	Met
4	5	Phe	His	Lys	Ser 180	Leu	Pro	His	Asp	Glu 185	Leu	Gly	Gln	Val	Thr 190	Ala	Asp
_	0	Asp	Phe	Ala 195	Ile	Leu	Glu	Asp	Cys 200	Ile	Leu	Asn	Gly	Asp 205	Phe	Ser	Ile
3	0	Cys	Glu 210	Asp	Val	Pro	Ala	Gly 215	Asp	Pro	Ala	Gly	Arg 220	Leu	Va1	Asn	Pro
5	5	Thr 225	Ala	Ala	Phe	Ala	Ile 230	Asp	Ile	Ser	Gly	Pro 235	Ala	Phe	Ser	Ala	Thr 240

Thr Ile Pro Pro Val Pro Thr Leu Ser Ser Pro Glu Leu Ala Ala Gln

(2) INFORMATION FOR SEQ ID NO:2:

250

255

Leu Ala Glu Leu Tyr Trp Met Ala Leu Ala Arg Asp Val Pro Phe Met 265 5 Gln Tyr Gly Thr Asp Glu Ile Thr Thr Thr Ala Ala Ala Asn Leu Ala 280 Gly Met Gly Gly Phe Pro Asn Leu Asp Ala Val Ser Ile Gly Ser Asp 10 295 Gly Thr Val Asp Pro Phe Ser Gln Leu Phe Arg Ala Thr Phe Val Gly 305 - 15 Val Glu Thr Gly Pro Phe Val Ser Gln Leu Leu Val Asn Ser Phe Thr Ile Asp Ala Ile Thr Val Glu Pro Lys Gln Glu Thr Phe Ala Pro Asp <u>.</u> ₡20 Leu Asn Tyr Met Val Asp Phe Asp Glu Trp Leu Asn Ile Gln Asn Gly 355 360 Gly Pro Pro Ala Gly Pro Glu Glu Leu Asp Glu Glu Leu Arg Phe Ile 7 25 30 Arg Asn Ala Arg Asp Leu Ala Arg Val Ser Phe Val Asp Asn Ile Asn 385 Thr Glu Ala Tyr Arg Gly Ser Leu Ile Leu Leu Glu Leu Gly Ala Phe Į, Ser Arg Pro Gly Ile Asn Gly Pro Phe Ile Asp Ser Asp Arg Gln Ala 420 425 430 35 Gly Phe Val Asn Phe Gly Thr Ser His Tyr Phe Arg Leu Ile Gly Ala Ala Glu Leu Ala Gln Arg Ala Ser Cys Tyr Gln Lys Trp Gln Val His 40 Arg Phe Ala Arg Pro Glu Ala Leu Gly Gly Thr Leu His Asn Thr Ile 465 470 45 Ala Gly Asp Leu Asp Ala Asp Phe Asp Ile Ser Leu Leu Glu Asn Asp 490 Glu Leu Leu Lys Arg Val Ala Glu Ile Asn Ala Ala Gln Asn Pro Asn 50 Asn Glu Val Thr Tyr Leu Leu Pro Gln Ala Ile Gln Val Gly Ser Pro 520 Thr His Pro Ser Tyr Pro Ser Gly His Ala Thr Gln Asn Gly Ala Phe 55 Ala Thr Val Leu Lys Ala Leu Ile Gly Leu Asp Arg Gly Gly Glu Cys

245

	545					550					555					560
5	Phe	Pro	Asn	Pro	Val 565	Phe	Pro	Ser	Asp	Asp 570	Gly	Leu	Glu	Leu	Ile 575	Asn
-	Phe	Glu	Gly	Ala 580	Cys	Leu	Thr	Tyr	Glu 585	Gly	Glu	Ile	Asn	Lys 590	Leu	Ala
10	Val	Asn	Val 595	Ala	Phe	Gly	Arg	Gln 600	Met	Leu	Gly	lle	His 605	Tyr	Arg	Phe
	Asp	Gly 610	Ile	Gln	Gly	Leu	Leu 615	Leu	Gly	Glu	Thr	Ile 620	Thr	Val	Arg	Thr
15	Leu 625	His	Gln	Glu	Leu	Met 630	Thr	Phe	Ala	Glu	Glu 635	Ala	Thr	Phe	Glu	Phe 640
<u> </u>	Arg	Leu	Phe	Thr	Gly 645	Glu	Val	Ile	Lys	Leu 650	Phe	Gln	Asp	Gly	Thr 655	Phe
20 E F F 25	Ser	Ile	Asp	Gly 660	Asp	Met	Cys	Ser	Gly 665	Leu	Val	Tyr	Thr	Gly 670	Val	Ala
25 []	Asp	Cys	Gln 675	Ala												
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